

## SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

### STAFF USE ONLY

Date completed: 10/24/82  
Searcher: DAVID L. GRIFFIN  
Terminal time: 2:00  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 2:30  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

**Search Site**  
\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S  
**Type of Search**  
\_\_\_\_ N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

**Vendors**  
\_\_\_\_ IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
\_\_\_\_ Other CCO

the 'information' and 'communication' fields. The 'information' field is defined as:

...the study of the nature, sources, uses, and management of information, and the study of the communication of information. (p. 1)

The 'communication' field is defined as:

...the study of the nature, sources, uses, and management of communication, and the study of the communication of information. (p. 1)

These definitions are not mutually exclusive, and the two fields overlap significantly.

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## SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
1	1947	100.0	347	AA113369	Acetic acid sequence
2	1947	100.0	347	AA180217	Human ER-229 protein
3	1943	99.8	347	AA062000	Human scavenger receptor
4	1939	99.6	347	AA064537	Human liver cell
5	721	37.0	3785	AA064591	Human SRC protein
6	719	36.9	422	AA064446	Human A144962-DEF
7	698	36.7	552	AA059417	Human STAT4-2-DEF
8	691.5	35.5	1453	AA065017	Human STAT4-2-DEF
9	690	35.4	1419	AA065040	Human TAPC-234
10	686	35.4	1413	AA065039	Human TAPC-234
11	686	35.2	1411	AA039493	Human TAPC-234

# Symplectic

## RESULT

694 4 469

1.2. *Wavelength*

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KW abn.

KW fiber

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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17-6

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PR 18 SEP 1997; 9708-0059463;  
 PR 18 SEP 1997; 9708-0059466;  
 PR 15 OCT 1997; 9708-0062295;  
 PR 17 OCT 1997; 9708-0062285;  
 PR 17 OCT 1997; 9708-0062287;  
 PR 21 OCT 1997; 9708-0063486;  
 PR 24 OCT 1997; 9708-0062814;  
 PR 24 OCT 1997; 9708-0062816;  
 PR 24 OCT 1997; 9708-0063455;  
 PR 24 OCT 1997; 9708-0063120;  
 PR 24 OCT 1997; 9708-0063121;  
 PR 24 OCT 1997; 9708-0063122;  
 PR 24 OCT 1997; 9708-0063124;  
 PR 27 OCT 1997; 9708-0063433;  
 PR 27 OCT 1997; 9708-0063427;  
 PR 27 OCT 1997; 9708-0063441;  
 PR 28 OCT 1997; 9708-0063442;  
 PR 28 OCT 1997; 9708-0063443;  
 PR 28 OCT 1997; 9708-0063449;  
 PR 28 OCT 1997; 9708-0063453;  
 PR 28 OCT 1997; 9708-0063456;  
 PR 28 OCT 1997; 9708-0063458;  
 PR 29 OCT 1997; 9708-0063704;  
 PR 29 OCT 1997; 9708-0063712;  
 PR 29 OCT 1997; 9708-0063738;  
 PR 29 OCT 1997; 9708-0063744;  
 PR 29 OCT 1997; 9708-0064215;  
 PR 29 OCT 1997; 9708-0063738;  
 PR 31 OCT 1997; 9708-0063870;  
 PR 31 OCT 1997; 9708-0064133;  
 PR 03 NOV 1997; 9708-0064248;  
 PR 07 NOV 1997; 9708-0064905;  
 PR 12 NOV 1997; 9708-0065186;  
 PR 17 NOV 1997; 9708-0065446;  
 PR 18 NOV 1997; 9708-0065563;  
 PR 21 NOV 1997; 9708-0066120;  
 PR 21 NOV 1997; 9708-0065454;  
 PR 24 NOV 1997; 9708-0066372;  
 PR 24 NOV 1997; 9708-0066366;  
 PR 24 NOV 1997; 9708-0066770;  
 PR 24 NOV 1997; 9708-0066511;  
 PR 24 NOV 1997; 9708-0066453;  
 XX  
 XX  
 XX (GENE) GENESER INC.  
 PR Chen J, Goddard A, Gurney AL, Pontica D, Wood WL, Yoon Y.  
 PR WPL 1999-02-02-0216  
 PR N-USDB: AAX52240.  
 PR Now isolated human genes and polypeptides used in the treatment of  
 PR gastrointestinal atrophy  
 PR Claim 12: FIG 54; 32pp; English.  
 XX  
 XX AAY13444 403 residues; secreted and transmembrane human proteins.  
 XX The cDNA sequences are obtained from cDNA libraries, prepared from  
 XX total lung, total kidney, total brain, total liver and total testis.  
 XX The encoded polypeptides have specific uses based on their homology to  
 XX known polypeptides, e.g., ppe211 and ppe217 can be used for ligands  
 XX associated with the preservation and maintenance of gastrointestinal  
 XX mucosa and the repair of acute and chronic mucosal lesions  
 XX (e.g., enterocolitis, Zollinger-Ellison syndrome, gastrinomas and  
 XX ulceration and congenital microvillus atrophy), skin diseases associated  
 XX with abnormal keratinocyte differentiation (e.g., psoriasis), epithelial  
 XX cancers such as lung squamous cell carcinoma of the ovary and pituitary,  
 XX potent effects on cell growth and development, diseases related to  
 XX growth or survival of nerve cells including Parkinson's disease,  
 XX Alzheimer's disease, ALS, neuropathies or cancer; ppe265 can be used as  
 XX for fibronectin, e.g. for reducing dermal scarring. ppe264 can be used  
 XX as a target for anti-tumor drugs; ppe513 may be used in the treatment  
 XX of Usher Syndrome or Ataxia telangiectasia; ppe266 can be used as an  
 XX anti-thrombotic agent; ppe287 polypeptides and portions may have

CC therapeutic applications in wound healing and tissue repair; ppe017 can  
 CC be used for treating problems of the kidney, uterus, endometrium, blood  
 CC vessels, or related tissue, e.g. in the heart or dental tract.  
 XX  
 XX Sequence 347 AA;  
 QQ  
 Query Match 100.0%; Score 1947; L6 20; Length 447;  
 Best local Similarity 100.0%; Pred. No. 146 153;  
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALPSELALATKTPPLASVSVRLVLAHNGRGGVAVLPSQWVYLSWLEKAVAV 60  
 RB 1 MALPSELALATKTPPLASVSVRLVLAHNGRGGVAVLPSQWVYLSWLEKAVAV 60  
 PR 1 MALPSELALATKTPPLASVSVRLVLAHNGRGGVAVLPSQWVYLSWLEKAVAV 60  
 QY 61 LQFELPDAASSTFSSSTLLEPAAEFFLVLSVSTGTGHTLAPQGEFVYLSHDELA 120  
 RB 61 LQFELPDAASSTFSSSTLLEPAAEFFLVLSVSTGTGHTLAPQGEFVYLSHDELA 120  
 PR 61 LQFELPDAASSTFSSSTLLEPAAEFFLVLSVSTGTGHTLAPQGEFVYLSHDELA 120  
 QY 121 QASVLRHSSISLVLSVLAELRGRKGVAVLRNGWVYLSWLEKAVAVRGLG 180  
 RB 121 QASVLRHSSISLVLSVLAELRGRKGVAVLRNGWVYLSWLEKAVAVRGLG 180  
 PR 121 QASVLRHSSISLVLSVLAELRGRKGVAVLRNGWVYLSWLEKAVAVRGLG 180  
 QY 181 GFAVLTEEPKRYAYGRFTIMLSWSSSEFATLVQVTPSWYVHTTHHDEHWPED 240  
 RB 181 GFAVLTEEPKRYAYGRFTIMLSWSSSEFATLVQVTPSWYVHTTHHDEHWPED 240  
 PR 181 GFAVLTEEPKRYAYGRFTIMLSWSSSEFATLVQVTPSWYVHTTHHDEHWPED 240  
 QY 241 LQFELPDAASSTFSSSTLLEPAAEFFLVLSVSTGTGHTLAPQGEFVYLSHDELA 300  
 RB 241 LQFELPDAASSTFSSSTLLEPAAEFFLVLSVSTGTGHTLAPQGEFVYLSHDELA 300  
 PR 241 LQFELPDAASSTFSSSTLLEPAAEFFLVLSVSTGTGHTLAPQGEFVYLSHDELA 300  
 QY 301 YGRVGRIMLVNRSCHQSLSQVQRIHWGHTHDEHVAVRSV 347  
 RB 301 YGRVGRIMLVNRSCHQSLSQVQRIHWGHTHDEHVAVRSV 347  
 PR 301 YGRVGRIMLVNRSCHQSLSQVQRIHWGHTHDEHVAVRSV 347  
 RESULT 2  
 ID AAB80237 standard; Protein: 347 AA.  
 XX  
 AC AAB80237;  
 XX  
 XX 24-APR-2001 (first entry)  
 XX  
 XX Human ppe229 protein.  
 XX  
 KW Human; ppe0; dermatological; antiproliferative; cytostatic; antiinflammatory;  
 KW antiangiogenic; vasodilator; neuroprotective; vulnerrary; cardiac;  
 KW antiarthritic; antihypertensive; antidiabetic; antitumor; cancer;  
 KW epithelial; antiinfective; antidiabetic; antitumor; cancer;  
 KW ischaemia; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Wo200104311-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 XX 22-APR-2000; 1999W-US04414.  
 XX  
 PR 07-JUL-1999; 99US-0140048;  
 PR 26-JUL-1999; 99US-0140698;  
 PR 28-JUL-1999; 99US-0140222;  
 PR 08-SEP-1999; 99W-US20594;  
 PR 13-SEP-1999; 99W-US20944;  
 PR 15-SEP-1999; 99W-US21090;  
 PR 15-SEP-1999; 99W-US21547;  
 PR 05-OCT-1999; 99W-US20899;  
 PR 29-NOV-1999; 99W-US28214;  
 PR 30-NOV-1999; 99W-US28313;  
 PR 16-DEC-1999; 99W-US30095;  
 PR 20-DEC-1999; 99W-US30911.











XX PS Claim 8; Fig 2; 459pp; English.

XX PA The present invention relates to TANGO or INTERCEPT proteins and coding

CC sequences (see AAF45121-F45136 and AAF45138-F45149 and AAB66041-B66057,

CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding

CC sequences are useful for the treatment of neurological disorders, local

CC central nervous system (CNS) disorders, CNS-related disorders, focal

CC brain disorders, global-diffuse cerebral disorders and other

CC neurological and cerebrovascular disorders. The CNS disorders include

CC Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic

CC lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,

CC autonomic function disorders such as hypertension and sleep disorders,

CC neuropsychiatric disorders, psychomotor substance use disorders,

CC anxiety, and bipolar affective disorder.

XX PS Claim 8; Pages 281-287; 459pp; English.

XX PS The present invention relates to TANGO or INTERCEPT proteins and coding

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CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding

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CC brain disorders, global-diffuse cerebral disorders and other

CC neurological and cerebrovascular disorders. The CNS disorders include

CC Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic

CC lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,

CC autonomic function disorders such as hypertension and sleep disorders,

CC neuropsychiatric disorders, psychomotor substance use disorders,

CC anxiety, and bipolar affective disorder.

XX PS Sequence 1319 AA;

50 Query Match 35.54; Score 691.5; DB 22; Length 1454;

51 Best Local Similarity 42.5%; Pred. No. 1,86-48;

52 Matches 139; Conservative 39; Mismatches 13; Indels 16; Caps 6;

53 4 LFS-----LITATCTPCTPLASPC-----VRVQCHLHRCRQSVVVEKRWQVYDQ 52

54 21 LLSVTELLINS- LLSSTGTDLLRITMDAQASQVQVPTPTDQ 74

55 53 WIKIVAVLPELQMAASTRESNIVFEAEFQVVSQVSTGRLHRTGKRNKRN 110

56 77 WLTASTQKQVPTQFQAS---TFTQATGATGKIKLHDSYQNSQWQEQH 144

57 111 VQDQREHLAGVTHPTSFPTVPRVFACHTERTDIAVPLALVAVLQADAS 150

58 134 SINCYNQETVQ- YQALPTLQDINQSRNKKLKKRQATLHQA 187

59 171 AARVCFQCTGCAVLTGFFCFKATCFETLNSQWATGKALQSS-SSQVQV 210

60 188 TAAVPTLPSSSTISSQNSPVLTPGKQILTPQSLQSLQVPLPQFQ 246

61 231 FCTVWEHRTD LRAVGHNCSSEPLVHRTVQVQVLEAWGFEKAVV 269

62 247 LQVTLVYSSSLCTFVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 310

63 289 KLELRECFKCYGVGVVGLHNVGSRQSQSEVQVQVQVQVQVQVQVQV 347

64 307 TAL-HLQPLQSQSDVGLQVQSQSQSTLWTRHSTQNTPLQPLQVGL 402

65 RESULT 9

66 AAB66040

67 ID AAB66040 standard; Protein: 1419 AA.

68 XX

69 AC AAB66040;

70 XX

71 DT 30-MAR-2001 (first entry)

72 DE Human TANGO 234 extracellular domain.

73 XX

74 KW TANGO protein; INTERCEPT protein; neurological disorder;

75 KW central nervous system; focal brain disorder; bipolar affective disorder;

76 KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;

77 KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;

78 KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;

79 KW neuropsychiatric; psychomotor substance use; anxiety.

80 OS Homo sapiens.

81 PN W020307239-A2.

82 XX

83 PD 21-DEC-2000.

84 XX

85 PF 24-MAY-2000; 2000W-US14859.

86 XX

87 14-JUN-1999; 990S-0343159.

88 XX (MILL-) MILLENNIUM PHARM INC.

89 XX McCarthy SA, Fraser CC, Sharp JD, Barnes TM;

90 XX WPI; 2001-034315/04.

91 PT TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for

92 screening assays and diagnostic assays and for the treatment of

93 neurological diseases such as Alzheimer's, Parkinson's and Huntington's

94 disease.

95 PS Claim 8; Pages 281-287; 459pp; English.

96 XX The present invention relates to TANGO or INTERCEPT proteins and coding

97 sequences (see AAF45121-F45136 and AAF45138-F45149 and AAB66041-B66057,

98 AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding

99 sequences are useful for the treatment of neurological disorders, local

100 brain disorders, global-diffuse cerebral disorders and other

101 neurological and cerebrovascular disorders. The CNS disorders include

102 Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic

103 lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,

104 autonomic function disorders such as hypertension and sleep disorders,

105 neuropsychiatric disorders, psychomotor substance use disorders,

106 anxiety, and bipolar affective disorder.

107 XX Sequence 1319 AA;

108 241 Match 35.14; Score 590; DB 22; Length 1419;

109 Best Local Similarity 42.5%; Pred. No. 1,86-48;

110 Matches 139; Conservative 39; Mismatches 13; Indels 16; Caps 6;

111 4 VLVQVHRCRQSVVVEKRWQVYDQ-----VRVQCHLHRCRQSVVVEKRWQVYDQ 83

112 8 LLSVTELLINS- LLSSTGTDLLRITMDAQASQVQVPTPTDQ 141

113 54 LFFQVGLVAVTGTGFFCFKATCFETLNSQWATGKALQSS-SSQVQV 201

114 57 LTPHPLQVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 118

115 143 LQVTLVYSSSLCTFVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 201

116 159 HNSQSRQSQSEVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 177

117 202 WLSQVHRCRQSVVVEKRWQVYDQ-----VRVQCHLHRCRQSVVVEKRWQVYDQ 259

118 178 LLDLQVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 247

119 240 LRAVGHNCSSEPLVHRTVQVQVLEAWGFEKAVV 269

120 248 KLELRECFKCYGVGVVGLHNVGSRQSQSEVQVQVQVQVQVQVQV 295

121 320 QSLQVHRCRQSVVVEKRWQVYDQ-----VRVQCHLHRCRQSVVVEKRWQVYDQ 346

122 296 SLVQVHRCRQSVVVEKRWQVYDQ-----VRVQCHLHRCRQSVVVEKRWQVYDQ 322

123 RESULT 10

124 AAB66039

125 ID AAB66039 standard; Protein: 1413 AA.

126 XX

127 AC AAB66039;

128 XX

129 DT 30-MAR-2001 (first entry)

130 DE Human TANGO 234 mature protein.

131 XX

132 KW TANGO protein; INTERCEPT protein; neurological disorder;

133 KW central nervous system; focal brain disorder; bipolar affective disorder;

134 KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;

KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;  
 KW Parkinson's; Gilles de la Tourette's syndrome; hypotension; sleep;  
 KW neuropsychiatric; psychoactive substance use; anxiety;  
 XX  
 CS Homo sapiens.  
 XX WO200077249 A2.  
 XX 21 DEC 2000.  
 XX 24 MAY 2001; WO 00/41757.  
 XX 14 JUN 1999; 9405 034315.  
 XX (MILL.) MILLENNIUM PHARM INC.  
 XX  
 PT McCarthy SA, Fraser CC, Sharp JD, Barnes TM;  
 XX WPI; 2001-032415/04.  
 XX  
 DR TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for  
 PT screening assays and diagnostic assays and for the treatment of  
 PT neurological diseases such as Alzheimer's, Parkinson's, Huntington's,  
 PT disease.  
 XX  
 CS Claim 8; pages 276-281; (5pp); English.  
 XX  
 CS The present invention relates to TANGO and INTERCEPT proteins and coding  
 CC sequences (see: AA045121, E45136, and AA045138, E45139, and AA045140, E45141,  
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Result No.	Query Match	Score	Length	DB	ID	Description	
1	1938	99.5	336	3	US-09-341-916-3	Sequence 3, April	
2	721	37.0	1705	4	US-09-341-987-3	Sequence 3, April	
3	589	20.2	332	3	US-09-034-916-4	Sequence 4, April	
4	585	30.1	102	3	US-09-034-916-5	Sequence 5, April	
5	582.5	29.9	1290	1	US-08-476-999-2	Sequence 2, April	
6	553	28.4	101	3	US-09-034-916-3	Sequence 3, April	
7	480	24.7	753	3	US-09-276-453-2	Sequence 2, April	
8	480	24.7	753	4	US-09-448-076-2	Sequence 2, April	
9	475	24.4	666	4	US-09-341-987-1	Sequence 1, April	
10	463.5	23.48	764	4	US-09-276-400-8	Sequence 8, April	
11	463.5	23.28	764	4	US-09-418-076-9	Sequence 8, April	
12	453.5	22.23	774	4	US-09-476-406-7	Sequence 7, April	
13	453.5	22.3	774	4	US-09-448-076-7	Sequence 7, April	
14	285	14.6	100	3	US-09-034-916-15	Sequence 15, April	
15	282	14.5	100	3	US-09-034-916-17	Sequence 17, April	
16	279	14.3	100	3	US-09-034-916-10	Sequence 10, April	
17	265	12.7	100	3	US-09-034-916-11	Sequence 11, April	
18	260.5	13.4	495	2	US-08-794-795-2	Sequence 2, April	
19	260.5	13.4	495	4	US-09-249-200-2	Sequence 2, April	
20	260.5	13.4	520	2	US-08-794-795-6	Sequence 6, April	
21	250.5	13.4	520	4	US-09-249-200-6	Sequence 6, April	
22	248.5	13.3	451	1	US-08-154-365-2	Sequence 2, April	
23	254.5	13.1	101	3	US-09-034-916-9	Sequence 9, April	
24	252.5	13.0	451	1	US-08-453-117-2	Sequence 2, April	
25	252.5	13.0	451	2	US-09-349-252-2	Sequence 2, April	
26	252.5	13.0	451	2	US-08-973-145-2	Sequence 2, April	
27	252.5	13.0	451	4	US-09-276-453-10	Sequence 10, April	

nearly Match. 99.58, 3 sets 1338, DB 3; Length 346;  
 Best local Similarity 100.0%; Prod. No. 2.7C-177;  
 Matches 345, Conservative 0, Mismatch 0, Indels









RESULT 10  
 US-04-276-40 : 8  
 : Sequence 8, Application US/09276400  
 : Patent No. 4140056  
 : GENERAL INFORMATION:  
 : APPLICANT: Khodadoust, Mehran  
 : TITLE OF INVENTION: NVEL MSP-18 PROTEIN AND NUCLEIC ACID SEQUENCES AND  
 : TITLE OF INVENTION: USES THEREOF  
 : FILE REFERENCE: MNI-074  
 : CURRENT AFFILIATION NUMBER: US 04-276-400

[illegible]









Source: human

Species: Homo sapiens (man)

Date: 11-Dec-2001 #sequence\_recid=11 Jan 2001 #at\_date=11 Jan 2001

Accession: A59486

Length: 77

Submitted to the Protein Sequence Database, March 2001

Accession number: A59486

Status: Preliminary

Molecule type: Protein

Protein name: 142721

Query Match 47.4% Score 726.53 DB 27 Length 240

Best Local Similarity 41.4% Prod No 140-45

Mismatches 147; Conservative 30; Mismatches 147; Indels 99; Gaps 63

QY 20 SPSTPMPVQRTBRRGKVPVQFQWVIVTQWQKRWAVTQWQGAASQDSYV 79

DB 480 SSALAKLVAGKGRGQGVAVETVKGWGIIVLQWRTGAAVTCQGLQWALANWAF 99

QY 40 PPPAFKQVLTQVSSVLTGDDLAQEQEE--VYDSSHDAASQENFESFVPPED 147

DB 540 ---QSSGPVLDVAVRGKRSYVSWSPHNTWLSHNGHSHDAVICSSESLA 54

QY 148 VRLALMTREDEVENSRHLEWLVVLRWLSLAAAVVLRWLSLAAV 147

DB 592 LQVAVNQRKQVQVIVYPQWVLTQWQRTGAAVTCQGLQWALANWAF 147

QY 198 RPPVWLSQMSVSGFATLQGPSWPKNTNIDEITWPT 248

DB 651 SGPVLDVAVRGKRSYVSWSPHNTWLSHNGHSHDAVICSSESLA 710

QY 249 ---EAPRDLRVAQVNDLQSGKRVLEKRWKAVVLRWLSLAAV 241

DB 711 PPGVAVSSSSVLLGVPRSSKQCGVIVLYGQWVQWVQWVQWVQWVQWV 779

QY 292 SPSTPMPVQRTBRRGKVPVQFQWVIVTQWQKRWAVTQWQGAASQDSYV 47

DB 791 GAPVQARVLSLQVAVVQWVQWVQWVQWVQWVQWVQWVQWVQWV 54

RESULT 4

142721

Species: Mus musculus (house mouse)

Date: 11-Jan-2000 #sequence\_recid=11 Jan 2000 #at\_date=11 Jan 2001

Accession: T42721

ReCheng, H.; McKee, M.; Chen, H.

Anal. Rec. 244, 327-343, 1996

Accession: 060 db 2000 #sequence\_recid=11 Jan 2000 #at\_date=11 Jan 2001

Accession number: T42721

Status: Preliminary

Molecule type: mRNA

Accession: 142721

Accession: 142721

Accession: 142721

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Query Match 26.98; Score 523; DB 2; Length 496;  
 Best Local Similarity 37.58; Pred. No. 3.7e-42;  
 Matches 129; Conservative 41; Mismatches 136; Indels 48; Gaps 12;

QY 24 VLVVGLHRCGRVVEVVKGGWGLVGDIGWIKIVAVIGRRLGAGAASGI PSGLL 78  
 DB 45 VLLTNSSSSGTVVHVRLEASWEPAGCALNIUSRAAAVTRALAGAGAAASGLAPTEL 104  
 QY 74 VFPFAAGGAVLLIG -----SVSLGELERLLAVRGGKYYDSHF EGNAAAT ENPES 129  
 DB 105 PPRPAARHLVAARATLAAAFALGLGAEKRL -GEVE HATRGPRKAPVFAIN- 158  
 QY 130 SPEVVEKRAADLGHFYFVIVVEHNEWYVLTWSSLEAAKVV-VGLDSEAEALVLEK 189  
 DB 159 -----RALRLVDGGACAGRVEMLEHGEMSGVGDITWLEDAIIVV-KGLDGRWAV -QA 210  
 QY 150 ECKKH-AVGRKPIWLSOMSCSREATIQDCISGPGWCKNTNHHEDTWVEGRLITLKLVA 248  
 DB 211 LPSLHFTPGRIHROGVNCSAAAYLWDFELD-GSHVYGRHFAVAVVYHGGWELLG 279  
 QY 249 GNLGANNRIIVYHGVWVSCTENWKEKEDVAVVKKQLSDN-----PSLSSEKRWKQVY 302  
 DB 270 GADQFTGVVVEFGVWNTVCGSWLVEEAKVLDGLGGLGDIATVAKKALMAGNSGKNVY 329  
 QY 303 PGVGRIMLDNVRCSEGEOSLEQCOHRTFWGFDICTHQEDVAVICS 346  
 DB 340 -----CNGELILSNCSWRFNNSNLSOSLAARVICS 361

RESULT 15  
 149100  
 mscd precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: 149100  
 R:Whitney, G.; Bowen, M.; Neubauer, M.; Aruffo, A.  
 Mol. Immunol. 32, 89-92, 1995  
 A:Title: Cloning and characterization of murine C16.  
 A:Reference number: 149100; MUID:95174761  
 A:Accession: 149100  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-626 <RES>  
 A:Cross-references: EMBL:012434; NID:3761719; FID:AAAG4667.1; U14:4761720  
 A:Genetics: Cd5  
 C:Superfamily: scavenger receptor cysteine-rich domain homology  
 F:42-155/Domain: scavenger receptor cysteine-rich domain homology <SR>  
 F:157-259/Domain: scavenger receptor cysteine rich domain homology <SR2>  
 F:261-360/Domain: scavenger receptor cysteine rich domain homology <SR3>

Query Match 21.48; Score 474.5; DB 2; Length 426;  
 Best Local Similarity 33.18; Pred. No. 2.7e-28;  
 Matches 117; Conservative 49; Mismatches 122; Indels 67; Gaps 13;

QY 24 GVRVWGLHRCGRVVEVVKGGWGLVGDIGWIKIVAVIGRRLGAGAASGI PSGLL 78  
 DB 44 GTRVNGSSRGSGVKVLEL-SWEPVAAHWNRAATLAVKALNFGUSGAVVLMPTSE 102  
 QY 68 GAASHPES 11VEPPAKKQKVLIGSVSCRTEDITLAQFQEEVYKSHED 119  
 DB 104 LPPATLSNTSSAGNTWAHAPIR-----CGANKQPKVQDGE-----SSSRKL 149  
 QY 124 AGAAG-ENGHSSEGVVVEVFLASQSGEVEVLVVEHGNWYVLTWSSLEAAKVV-VGLDSEAEALVLEK 189  
 DB 150 VVVFCAEN-----QAVRLVGGSSKACAGVEMLEHGEMSGVGDITWLEDAIIVV-KGLDGRWAV -QA 210  
 QY 179 LQGPVAVITQFQKPH AVCEKPIWLSOMSCSREATIQDCISGPGWCKNTNHHEDTWVEGRLITLKLVA 248  
 DB 201 LKGSWAV--KALAGLHFTPGRIHROGVNCSAAAYLWDFELD-GSHVYGRHFAVAVVYHGGWELLG 279

Search completed: August 20, 2002, 14:00:49  
 Job time: 14 sec

QY 249 GPEPRLRLWQENLQASQPLEVLEHFAVWGSVVRNINCEFEFAVVKQLQDSEFSL----- 292  
 DB 258 CSSEHLSWPLDGLDSDSCVQVVEVFPVWSIVTDSWYTPSEAFVLCESTLGGSAVAPRGL 317  
 QY 293 PSPEDEKCKYGPVVRHILINVR-SSEFEQSLEAFQDHFHWZHHWTHGHAVAVICS 346  
 DB 318 PHSLDGRMY-----YSCKGJFALSTGWSRFNNSNLSOSLAARVICS 360



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2002, 12:55:16, Search time 15.5 seconds  
(without alignments)  
1001.169 Million cell updates/seq

Title: US-09-904-462A-148

Perfect score: 1947

Sequence: 1 MALLPSLLHAIACIRGFIAS.....RFGPHDTHRHNAVIVSV 447

Scoring table:

BLASTOM62  
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000+000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	563	34.1	1436	1 WC11_BOVIN	p42062 Bos taurus
2	643	33.0	875	1 NEIR_HUMAN	p56740 Homo sapien
3	632	32.5	761	1 NPTR_MOUSE	p30792 Mus muscula
4	523	26.9	668	1 CD6_HUMAN	p40203 Homo sapien
5	480	24.7	753	1 LOL3_HUMAN	p58215 Homo sapien
6	468	24.1	665	1 GD6_MOUSE	p61003 Mus musculu
7	464.5	23.8	754	1 LOL3_MOUSE	p59413 Mus musculu
8	453.5	23.3	774	1 LGL2_HUMAN	p14264 st frondyloru
9	373.5	19.4	532	1 SPER_STRPU	p00004 Bos tauru
10	269.5	13.4	520	1 MKCQ_HUMAN	p21757 Homo sapien
11	264.5	13.2	459	1 MSRE_MOUSE	p05895 Cryptotolanu
12	262.5	13.0	451	1 MSRE_HUMAN	p21798 Bos tauru
13	252	12.9	454	1 MSRE_RALIT	p66754 Mus musculu
14	251	12.9	454	1 MSRE_BOVIN	p00004 Bos tauru
15	247.5	12.7	518	1 MTC9_MOUSE	p13377 Mus musculu
16	245	12.6	483	1 MKCQ_MESAU	p13377 Mus musculu
17	245.5	12.3	494	1 GD5_KAT	p53662 Rattus norv
18	226.5	11.9	491	1 GD5_KAT	p53662 Rattus norv
19	198	10.2	495	1 GD5_HUMAN	p04127 Homo sapien
20	189	9.7	495	1 GD5_BOVIN	p14238 Bos tauru
21	147	7.6	1113	1 COR1_MOUSE	p32419 Mus musculu
22	145.5	7.5	5376	1 ZAN_MOUSE	p00799 Mus musculu
23	138	7.1	469	1 PROP_HUMAN	p27918 Homo sapien
24	134	7.0	455	1 TMS5_MOUSE	p00104 Mus musculu
25	134.5	6.9	583	1 TMS5_HUMAN	p00156 Homo sapien
26	130	6.7	1746	1 TENA_PIG	p24116 Sus scrofa
27	127.5	6.5	1584	1 HALL_HUMAN	p14514 Homo sapien
28	125.5	6.4	4289	1 TENX_HUMAN	p22105 Homo sapien
29	124.5	6.4	1042	1 COR1_HUMAN	p09535 Homo sapien
30	121.5	6.2	4543	1 LRPI_CHICK	p04167 Gallus gall
31	121	6.2	1709	1 BAR3_WHITE	p04374 Chitracomus
32	121	6.2	4753	1 LRPI_WHITE	p04683 Canorolabadi
33	120.5	6.2	4460	1 LRPI_PA	p04683 Canorolabadi

34	118	6.1	1115	1 GPCR_TYMS	p46024 Lymnaea sta
35	117.5	6.0	1984	1 YL_DROME	p98163 Drosophila
36	117.5	6.0	3712	1 LMA_DROME	p00174 Drosophila
37	117	6.0	644	1 GROM_KAT	p27590 Rattus norv
38	115	5.9	860	1 ATSG_HUMAN	p00405 Homo sapien
39	113	5.8	640	1 GROM_HUMAN	p07911 Homo sapien
40	113	5.8	2201	1 TENA_HUMAN	p24821 Homo sapien
41	112	5.9	3672	1 TMS2_CAHLL	p21413 Canorolabadi
42	111.5	5.7	909	1 TML_XENIA	p09687 Xenopus lae
43	111.5	5.7	2871	1 FBNI_PIG	p51246 Sus scrofa
44	111.5	5.7	4544	1 LRPI_HUMAN	p07954 Homo sapien
45	111	5.7	593	1 GRN_HUMAN	p28749 H grandis

#### ALIGNMENTS

RESULT	1	WC11_BOVIN	STANDARD	PKT	1436 AA.
ID	WC11_BOVIN				
AC	P30205				
DT	01-APR-1993 (Rel. 25, Created)				
DT	01-APR-1993 (Rel. 25, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Antigen WC11 precursor.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Rovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
KP	SEQUENCE FROM N.A.				
KC	TISSUE=Blood;				
KX	MEDLINE=93056489; Pubmed 141105;				
RA	Wijnhoud P.H.J., Metzelaar M.J., Machoud N.D., Morrison W.L.,				
RA	Clevers H.C.;				
RT	"Molecular characterization of the WC1 antigen expressed specifically				
KL	on bovine CD4-CD8 gamma delta T lymphocytes";				
CC	J. Immunol. 149:3273-3277(1992).				
CC	1- SUBCELLULAR LOCATION: Secreted.				
CC	1- SIMILARITY: CONTAINS 11 SECR DOMAINS.				
CC	This SWISS PROT entry is copyrighted. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.ebi.ac.uk/submit/submit.html">http://www.ebi.ac.uk/submit/submit.html</a> )				
CC	or send an email to <a href="mailto:license@ebi.ac.uk">license@ebi.ac.uk</a> .				
CC	EMBL: X6723, 7661-7255, 1;				
CC	PIR: S19913; S19913.				
CC	PIR: A46496; A46496.				
CC	InterPro: IPR001190; SRCR.				
CC	Plant: PF005540; SRCR: 11.				
CC	PRINTS: PR09258; SPCRACR:TRFTR.				
CC	SMART: SM00202; SR: 11.				
CC	PROSITE: PS00420; SRCR: 1; 4.				
CC	PROSITE: PS0267; SRCR: 2; 11.				
CC	Antigen: Repeat; Glycoprotein; Signal.				
CC	FT SIGNAL	1	25	POTENTIAL.	
CC	FT CHAIN	26	1436	ANTIGEN WC1.1.	
CC	FT DOMAIN	18	131	SRCR 1.	
CC	FT DOMAIN	134	234	SRCR 2.	
CC	FT DOMAIN	239	340	SRCR 3.	
CC	FT DOMAIN	376	476	SRCR 4.	
CC	FT DOMAIN	481	581	SRCR 5.	
CC	FT DOMAIN	586	686	SRCR 6.	
CC	FT DOMAIN	689	789	SRCR 7.	
CC	FT DOMAIN	794	895	SRCR 8.	
CC	FT DOMAIN	931	1031	SRCR 9.	
CC	FT DOMAIN	1036	1136	SRCR 10.	
CC	FT DOMAIN	1155	1255	SRCR 11.	















```

CX 1 Strongly conserved.
CX NCBI_LaXID: 7658;
[+]
FN SEQUENCE FROM N.A., AND SEQUENTIAL OF 477 AA.
FX MEDLINE 98146152; PubMed 2529972;
FA Danqotti L.J., Jordan J.E., Bellet K.A., Barbiers J.,
K. "Cloning of the mRNA for the protein that crosslinks to the cat
peptide spectrin."
RL Proc. Natl. Acad. Sci. U.S.A. 86:2129-2132(1989).
CX 1 FUNCTION: RECEPTOR FOR THE EGF FETIDE SPECTIN.
CX 1 SUBCELLULAR LOCATION: Type 1 membrane protein.
CX 1 SIMILARITY: CONTAINS 4 SPOK DOMAINS.
CX
CX This SWISS-Prot entry is copyrighted. It is produced through a collaboration
CX between the Swiss Institute of Bioinformatics and the EMBL outstation
CX at the European Bioinformatics Institute. There are no restrictions on its
CX use by non-profit institutions as long as its content is in no way
CX modified and this statement is not removed. Usage by and for commercial
CX entities requiring a license agreement. See http://www.isb.ch/ for more info.
CX or send an email to license@isb.ch)
CX
FX EMBL: J04519; AAA0078; 1;
FX PIR: A42751; A42751;
FX InterPro: IPR001196; SPOK;
FX Pfam: PF00540; SPOK; 4;
FX PRINTS: PR00256; SPOK; 1; 4;
FX SMART: SM00202; SR; 4;
FX PROSITE: PS00420; SPOK; 1; 4;
FX PROSITE: PS00267; SPOK; 2; 4;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT CHAIN 1 40 EGF PEPTIDE SPECTIN RECEPTOR.
FT DOMAIN 1 30 EGF REPEATS (PROTEIN).
FT DOMAIN 2 31 40 EGF REPEATS (PROTEIN).
FT DOMAIN 3 41 52 EGF REPEATS (PROTEIN).
FT DOMAIN 4 53 64 EGF REPEATS (PROTEIN).
FT DOMAIN 5 65 76 EGF REPEATS (PROTEIN).
FT DOMAIN 6 77 88 EGF REPEATS (PROTEIN).
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FT DOMAIN 12 149 160 EGF REPEATS (PROTEIN).
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FT DOMAIN 55 665 676 EGF REPEATS (PROTEIN).
FT DOMAIN 56 677 688 EGF REPEATS (PROTEIN).
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FT DOMAIN 58 701 712 EGF REPEATS (PROTEIN).
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FT DOMAIN 61 737 748 EGF REPEATS (PROTEIN).
FT DOMAIN 62 749 760 EGF REPEATS (PROTEIN).
FT DOMAIN 63 761 772 EGF REPEATS (PROTEIN).
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FT DOMAIN 65 785 796 EGF REPEATS (PROTEIN).
FT DOMAIN 66 797 808 EGF REPEATS (PROTEIN).
FT DOMAIN 67 809 820 EGF REPEATS (PROTEIN).
FT DOMAIN 68 821 832 EGF REPEATS (PROTEIN).
FT DOMAIN 69 833 844 EGF REPEATS (PROTEIN).
FT DOMAIN 70 845 856 EGF REPEATS (PROTEIN).
FT DOMAIN 71 857 868 EGF REPEATS (PROTEIN).
FT DOMAIN 72 869 880 EGF REPEATS (PROTEIN).
FT DOMAIN 73 881 892 EGF REPEATS (PROTEIN).
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FT DOMAIN 86 1037 1048 EGF REPEATS (PROTEIN).
FT DOMAIN 87 1049 1060 EGF REPEATS (PROTEIN).
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FT DOMAIN 91 1097 1108 EGF REPEATS (PROTEIN).
FT DOMAIN 92 1109 1120 EGF REPEATS (PROTEIN).
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FT DOMAIN 110 1325 1336 EGF REPEATS (PROTEIN).
FT DOMAIN 111 1337 1348 EGF REPEATS (PROTEIN).
FT DOMAIN 112 1349 1360 EGF REPEATS (PROTEIN).
FT DOMAIN 113 1361 1372 EGF REPEATS (PROTEIN).
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FT DOMAIN 115 1385 1396 EGF REPEATS (PROTEIN).
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FT DOMAIN 123 1481 1492 EGF REPEATS (PROTEIN).
FT DOMAIN 124 1493 1504 EGF REPEATS (PROTEIN).
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FT DOMAIN 143 1721 1732 EGF REPEATS (PROTEIN).
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FT DOMAIN 145 1745 1756 EGF REPEATS (PROTEIN).
FT DOMAIN 146 1757 1768 EGF REPEATS (PROTEIN).
FT DOMAIN 147 1769 1780 EGF REPEATS (PROTEIN).
FT DOMAIN 148 1781 1792 EGF REPEATS (PROTEIN).
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FT DOMAIN 440 5285 5296 EGF REPEATS (PROTEIN).
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FT DOMAIN 445
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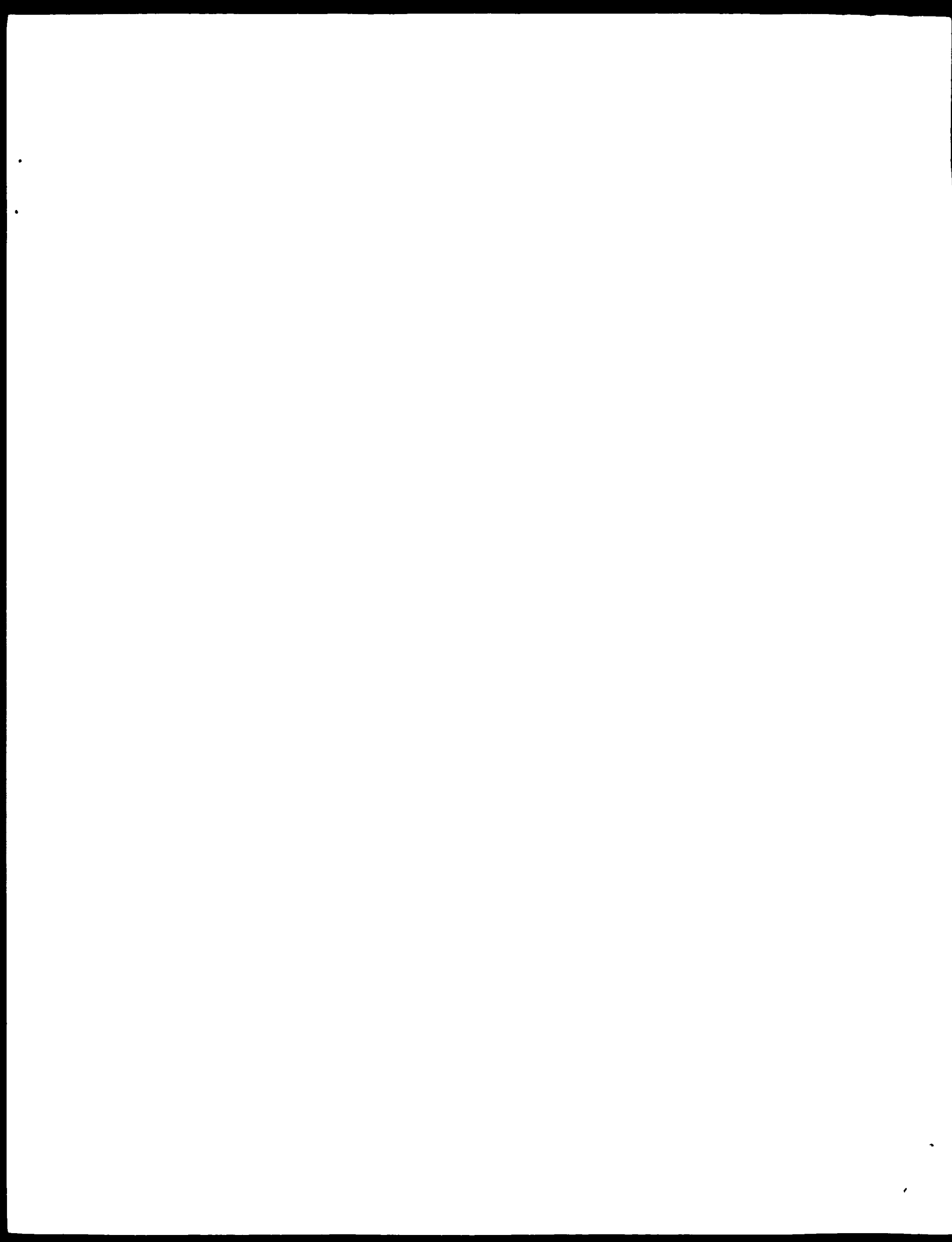












Result	No.	Score	Query		ID	Description
			Match	Length		
1	1943	99.8	347	4	043866	043866 homo sapien
2	1341	68.9	352	11	043500	043500 mus muscula
3	1341	68.9	352	11	043805	043805 mus muscula
4	1329	68.9	352	11	043807	043807 mus muscula
5	1326	68.1	352	11	043501	043501 mus muscula
6	822	42.2	470	13	043801	043801 gallus galli
7	754	36.7	1594	6	045218	045218 gallus gallus
8	737.5	37.9	2413	4	040834	040834 homo sapien
9	735.5	37.8	2412	4	040857	040857 homo sapien
10	734.5	37.7	2413	4	040834	040834 homo sapien
11	726.5	37.3	2403	4	040802	040802 homo sapien
12	724	37.3	2426	4	040803	040803 homo sapien
13	725	37.2	1785	4	043211	043211 homo sapien
14	722.5	37.1	1121	11	043808	043808 mus muscula
15	721	37.0	1785	4	043439	043439 homo sapien
16	709	36.4	1957	11	043803	043803 mus muscula









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Query Match          47.98; Score 737.5; DB 4; Length 2413;
Best Local Similarity 41.64; Pred. No. 26-60;
Matches 148; Conservative 28; Mismatches 119; Gaps 19; Gaps 7;

QY 20 SPSGRLVGLHREGRFVEVEKQKQWRTVDEGWLKQWAVDSEDEGAAASHTLSLLY 79
DB 496 SSIARLKLNGEHPGQGVLYFGSGWCVDSWMTLANNVCKLGLAMWMLAPNARF 549
QY 80 EPFAKFFKRVLLSVSTCTETELTAQHQEE--VYHSHIDEAASVETNDEPFDVDEG 147
DB 550 --GQSGPIVLHVRVSGNESYLWSPHNGWLSHNGGSHSDAIVTSGHSSLA-- 609
QY 138 VGLAZHFRHCEHAAVEELNATVAV--SKGLAAEVA--L--L--L--L--L--L--L-- 197
DB 602 LRLVNGHRCQGEVEVFEFGWGVTEGLGWTG--ARVVGELG--AAHAAEAT--L-- 660
QY 198 RKPIMLSMSVSGREAILQDPSGHWKNTGNIDEPTWVE--L--L--L--L--L--L--L-- 248
DB 661 SGPVIDIVVRSGHESYLWSPHNNWLSHNGGHHEDACVIGSAASSTPRPILSL 720
QY 239 -----RPPTHRLVGDNDLCSHLEVLHRCVWGSVCTENWGHKEGVYK--L--L--L-- 291
DB 721 PSTVTSSESTFLRANVSDIEFGKQVVEVLYKSGVCTVDSWTDINADVVRGLNGWAM 780
QY 292 SPSFGRKTYGAGVYKINLHVSGSGEFGSLKQGHSEFWGPHETLHAEVAVDGV 447
DB 781 SAGNAR--FUGSGPIVLDVRGSHSYLWSPHNGWLSHNGGHHEDACVIGSAAS 844

RESULT 9
Q96J57
ID Q96J57 PRELIMINARY; FRG, 2413 AA.
AC Q96J57
DT 01-MAY-2000 (Tremblere, 13, Created)
DI 01-MAY-2000 (Tremblere, 13, Last sequence update)
DE 01-DEC-2001 (Tremblere, 19, Last annotation update)
DE DMRT1/9KB 2 PROTEIN PRECURSOR.
GN DMRT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId 9606.
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE=TRACHEA.
RX MEDLINE 99415048; PubMed 10485905.
RA Reimskov U., Mollenhauer J., Kadane J., Virend L., Grandjean P.,
RA Tornero L., Klitem A., Reid K.B., Pousta A., Skjodt K.,
RA "Cloning of gp-340, a putative epstein receptor for lung carcinoma
RA protein D."
RL Prof. Natl. Acad. Sci. U.S.A. 96:10794-10799(1999).
CC 1- SIMILARITY: CONTAINS 2 CUB DOMAIN.
DR EMPL: A124-213; CAH56155.1.
DR HSER: P35327.1.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR001190; SRCR.
DR InterPro: IPR001507; zona_pellucida.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00530; SRCR; 14.
DR Pfam: PF01000; zona_pellucida; 1.
DR PRINTS: PR00258; SPERACTRIPR.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00202; SR; 14.
DR SMART: SM00241; ZP; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS00420; SRCR_1; ORDER_WIL_12.
DR PROSITE: PS00287; SRCR_2; 14.
DR PROSITE: PS00673; ZP_DOMAIN; ORDER_WIL_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 2413 AA; 26069 MW; 3F43C9D9E9D7E994.

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Query Match          47.78; Score 734.5; DB 4; Length 2413;
Best Local Similarity 39.88; Pred. No. 5.7e+60;
Matches 150; Conservative 42; Mismatches 108; Gaps 19; Gaps 7;

QY 11 DTPHSPLASIS-----GVPLVGGIHRCTEHRVEVEKQKQWRTVDEG 52
DB 332 TCSAPQSPTDPTWPTSHASTADPSSIALRLVNGSDRCQKQWVLYRGSWITWDOS 491
QY 53 WPKRIVAMVPELGGGAASCHTSGHLYEDPAKPEKVLGVSGCTHETLLAQHQEE-- 110
DB 392 WPKSARVVKGLSGWATSALGNAR--GGSSPFLVLAVRSGHSTLWSTLRHWL 448
QY 111 VYDSHIDEAASVETNDEPFDVDEG-----GVKLAPGHKQKVE 152
DB 449 SHNCGSHSDAIVTSGHSSLSSTPSDILPTLTPASTVSGSSSLALRLVNGSDRCQKVE 508
QY 153 VPKRQWTV--GV--WSTPAAPV--KGLG--KRAV--K--K--K--K--K--K--K--K-- 212
DB 509 VLYRGSWITVDSWTDINADVVRKGLSGWMLAPNAR--K--GSGSPFLVLAVRSGH 567
QY 214 AILQDPSGHWKNTGNIDEPTWVE--L--L--L--L--L--L--L--L--L--L--L-- 269
DB 568 SYLWSPHNGWLSHNGGSHSDAIVTSGHSSLSALRLVNGSDRCQKVEVLYRGSWITWD 627
QY 276 LNAVTPFTVAVV--GV--K--SIS--P--GV--V--V--V--V--V--V--V--V--V-- 629
DB 628 DSWHTIRAVVCKGLGQWMAEAFGNAR--K--GSGSPFLVLAVRSGHSTLRHWL 685
QY 330 WCHHETHTGTHAVTICS 446
DB 686 WLSHNGGHHEDACVIGS 702

RESULT 10
Q96J04
ID Q96J04 PRELIMINARY; FRG, 2413 AA.
AC Q96J04
DI 01-DEC-2001 (Tremblere, 19, Created)
DI 01-DEC-2001 (Tremblere, 19, Last sequence update)
DI 01-DEC-2001 (Tremblere, 19, Last annotation update)
DE DMRT1/9KB 2 PROTEIN PRECURSOR.
GN DMRT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId 9606.
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE.
RA Mollenhauer J.,
RA "Major subforms of DMRT1 are gastrointestinal mucins that display
RA extensive alternative splicing and differential protein targeting."
RA Schmitt J. (B. V. G.) 2001. In: PDB. 1999. 1999. 1999. 1999.
DR EMPL: A12475.1; CAH44122.1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 2413 AA; 26069 MW; 90A449C5F4F69726 CAC94;

Query Match          47.78; Score 734.5; DB 4; Length 2413;
Best Local Similarity 39.88; Pred. No. 5.7e+60;
Matches 150; Conservative 41; Mismatches 109; Gaps 19; Gaps 7;

QY 11 DTPHSPLASIS-----GVPLVGGIHRCTEHRVEVEKQKQWRTVDEG 52
DB 332 TCSAPQSPTDPTWPTSHASTADPSSIALRLVNGSDRCQKQWVLYRGSWITWDOS 491
QY 53 WPKRIVAMVPELGGGAASCHTSGHLYEDPAKPEKVLGVSGCTHETLLAQHQEE-- 110
DB 392 WPKSARVVKGLSGWATSALGNAR--GGSSPFLVLAVRSGHSTLWSTLRHWL 448
QY 111 VYDSHIDEAASVETNDEPFDVDEG-----GVKLAPGHKQKVE 152
DB 449 SHNCGSHSDAIVTSGHSSLSSTPSDILPTLTPASTVSGSSSLALRLVNGSDRCQKVE 508
QY 153 VPKRQWTV--GV--WSTPAAPV--KGLG--KRAV--K--K--K--K--K--K--K--K-- 212
DB 509 VLYRGSWITVDSWTDINADVVRKGLSGWMLAPNAR--K--GSGSPFLVLAVRSGH 567
QY 214 AILQDPSGHWKNTGNIDEPTWVE--L--L--L--L--L--L--L--L--L--L--L-- 269
DB 568 SYLWSPHNGWLSHNGGSHSDAIVTSGHSSLSALRLVNGSDRCQKVEVLYRGSWITWD 627
QY 276 LNAVTPFTVAVV--GV--K--SIS--P--GV--V--V--V--V--V--V--V--V--V-- 629
DB 628 DSWHTIRAVVCKGLGQWMAEAFGNAR--K--GSGSPFLVLAVRSGHSTLRHWL 685
QY 330 WCHHETHTGTHAVTICS 446
DB 686 WLSHNGGHHEDACVIGS 702

RESULT 11
Q96J04
ID Q96J04 PRELIMINARY; FRG, 2413 AA.
AC Q96J04
DI 01-DEC-2001 (Tremblere, 19, Created)
DI 01-DEC-2001 (Tremblere, 19, Last sequence update)
DI 01-DEC-2001 (Tremblere, 19, Last annotation update)
DE DMRT1/9KB 2 PROTEIN PRECURSOR.
GN DMRT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId 9606.
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE.
RA Mollenhauer J.,
RA "Major subforms of DMRT1 are gastrointestinal mucins that display
RA extensive alternative splicing and differential protein targeting."
RA Schmitt J. (B. V. G.) 2001. In: PDB. 1999. 1999. 1999. 1999.
DR EMPL: A12475.1; CAH44122.1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 2413 AA; 26069 MW; 90A449C5F4F69726 CAC94;

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[illegible]





